

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/573,999
Source: IFWP
Date Processed by STIC: 4/13/06

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/573,999

DATE: 04/13/2006

TIME: 10:01:02

Input Set : A:\BCS_03-5005_PCT-SEQUENZPROTOKOLL.ST25.txt
 Output Set: N:\CRF4\04132006\J573999.raw

3 <110> APPLICANT: Bayer CropScience GmbH
 5 <120> TITLE OF INVENTION: Plants with increased activity of a Class 3 branching enzyme
 7 <130> FILE REFERENCE: BCS 03-5005-PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/573,999
 C--> 9 <141> CURRENT FILING DATE: 2006-03-30
 9 <150> PRIOR APPLICATION NUMBER: EP 03090324.9
 10 <151> PRIOR FILING DATE: 2003-09-30
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1004
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Solanum tuberosum
 21 <400> SEQUENCE: 1
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 26 caagatgatc agattaatta catctacaat tggtggtcat gcatacctca acttcatggg 180
 28 caatgaattt ggtcacccaa agagagtaga gtttccaatg tcaagcaaca atttctcctt 240
 30 ttcaactggct aaccgtcgct gggatctatt ggaagatgtt gtacattatc aattgttctc 300
 32 atttgataag ggtatgatgg acttggataa aaatgggaga attttgtcca gaggtcttgc 360
 34 caacattcac catgtcaatg atactaccat ggtgatttct tacttgagag gtcccaatct 420
 36 ctttgttgc aactttcattc ctgtcaattc atatgaaaga tacattatag gtgtgaaaga 480
 38 agctggagag tatcaagtca cattaaatac agataaaaac aagtatggtg gttagaggact 540
 40 acttggccat gatcagaata ttcaaagaac cattagtaga agagctgatg gaatgagatt 600
 42 ttgcttggaa gtgcctctgc caagtagaaag tgctcaggct tacaagttga cccgaattct 660
 44 aagagcatga tcactctagt aatcaaagtg cctcatatga tgacacaaaaa ggaaaggttc 720
 46 tacattgccct ttacactgat caatattgac accttccga ggtgagttc tgtgattctt 780
 48 gagcagactg ttggctagtc aattatcatg aacttttgc ttcaagcatcc ggatagtcgc 840
 50 ttctcctgtg caatgagggc atggacgaat tttttttgg cttgtcatgg gggtcataag 900
 52 catccgccag attaagattt cacaggcctc gagtaaaacc atcaacttact ttaaggatac 960
 54 acaaacacac caacgggtg caggctctga taccttctaa agtg 1004
 57 <210> SEQ ID NO: 2
 58 <211> LENGTH: 2096
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Solanum tuberosum
 62 <400> SEQUENCE: 2
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 65 tagtttcta tctcaaacgg gaagcagaac cagtcggcag cttaaatttg ttgcgcagccg 120
 67 ccgggctcga gtttcgaggt gtatgtctc agcaacggag caaccgccac cgcaacgacg 180
 69 gaagcaacga ccggagaagt acaaacagtc ggaggaaggg aaaggaatcg atcctgttgg 240
 71 atttctcagc aaatacggca ttactcataa agcgttgcgta caatttcttc gtgaaagata 300
 73 taaatcattg aaggacttga aggatgaaat attgactcgat catttcagtc tcaaggagat 360
 75 gtctactggg tatgaattaa tgggtatgca tcgcaacata caacatcgag tggatttctt 420

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77 ggaatgggct ccaggtgctc gctactgtgc tctgattggt gacttcaatg ggtggtaac 480
 79 aactggtaac tgtccagag agggcattt tggcatgac gattatgggt attggttat 540
 81 tattcttcaa gataaattac gtgaaggaga agaacctgat aaattgtatt ttcaacagta 600
 83 caattatgcg gaggactatg gtaaaggta cacggattt accgtcgagg aaatcttaa 660
 85 aaaagcaaat gatgagttt gggAACCTGG agaagatgc ttcataaat cacgttatg 720
 87 ggtggcagca aagtatatg aggaaatgtt cggaccaat ggacctaaca cagaagagga 780
 89 actagaagca atgcctgtatc cagctacacg atacaaaact tggaaagagc aacaaaaaaga 840
 91 ggatccggca agcaatttgc catcgatgatc tggtagat agtggaaaag aatatgat 900
 93 ttacaatatt ataggtgatc ctgaatcgat taagaaattt cgtatgaaac agcctcctat 960
 95 tgcttactgg ttagaaacta aaaagggaaag gaaaggctgg ttacagaat atatgcctgc 1020
 97 tttacctcat ggaagcaaat acagggtgta ttttaacaca ccaaattggc ctctgtac 1080
 99 agttcctgcg tggccaatt ttgtcattcc agatgcaggc gggatggcat tagcagtcca 1140
 101 ttgggaacca cctcctgaat atgcttataa atggaaacac aagctaccag tcaagctaa 1200
 103 gtccttgcgc atatatgaat gtcatgttg catctctggc caggaacca aagtttcattc 1260
 105 tttcaatgtat tttatttagca aggtccttcc gcatgtaaaa gaagctggat acaatgcaat 1320
 107 acaaattatt ggagttgtt agcacaagga ttatttcact gttggatata gagtgacca 1380
 109 tttttatgct gtttagtagcc gttatggcac accggatgac ttcaagcgct tgggtatg 1440
 111 agcacatggg cttggactgc ttgtctttt ggagattgtg cactttatg cagcagcaga 1500
 113 tgaatgggtt gggttatctc ttttgcattt agcaatgtat tgctatttcc acactggtaa 1560
 115 acgtggacac cacaatttgc gggcacacg gatgttcaaa tatggagatc ttgtatgttct 1620
 117 gcactttctt cttcaaaatc tgaactgggtt ggtggaggag tatcatgtcg atgcttcca 1680
 119 ttttcatcg ctctcgatcca tggatgtatac gcataatggta tttgcttcatttactggta 1740
 121 catggatgaa tactgttacc aatatgttgc caaggaggcc ttattgtacc tcatttttttgc 1800
 123 aaatgaagta ttacatgctc ttcatcttgc tttgtatcacttgcatttgcatttgcatttgc 1860
 125 gtatcctggc ctctcgatc caacatctca aggtggactg ggctttgatt atttggccaa 1920
 127 tcttcgttgc tcagagatgtt ggcttgcatttgcatttgcatttgcatttgcatttgcatttgc 1980
 129 catgagtaag attgttagca cattatgtggg cgatagacaa aatactgata aaatgtttt 2040
 131 gtatgcagaa aatcacaacc agtccatttc tggaggtcgatccatcgatccatcgatccatcg 2096
 134 <210> SEQ ID NO: 3
 135 <211> LENGTH: 3204
 136 <212> TYPE: DNA
 137 <213> ORGANISM: Solanum tuberosum
 139 <220> FEATURE:
 140 <221> NAME/KEY: CDS
 141 <222> LOCATION: (99)..(2804)
 145 <400> SEQUENCE: 3
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 148 cggcaggatgttgc atggatatcttgc gcaatttcg gcttaaca atg ctc tct ctg tgc gat 116
 149 Met Leu Ser Leu Ser Asp
 150 1 5
 152 tca att cga att tct tca cca ttg agc gat tct cgt ctt agt ttt cta 164
 153 Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp Ser Arg Leu Ser Phe Leu
 154 10 15 20
 156 tct caa acc gga agc aga acc agt cgc cag ctt aaa ttt gtt cgc agc 212
 157 Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln Leu Lys Phe Val Arg Ser
 158 25 30 35
 160 cgc cgg gct cga gtt tcg agg tgg tgc tca gca acg gag caa ccg 260
 161 Arg Arg Ala Arg Val Ser Arg Cys Arg Cys Ser Ala Thr Glu Gln Pro
 162 40 45 50

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165	Pro	Pro	Gln	Arg	Arg	Lys	Gln	Arg	Pro	Glu	Lys	Tyr	Lys	Gln	Ser	Glu		
166	55							60									70	
168	gaa	gag	aaa	gga	atc	gat	cct	gtt	gga	ttt	ctc	agc	aaa	tac	ggc	att		356
169	Glu	Glu	Lys	Gly	Ile	Asp	Pro	Val	Gly	Phe	Leu	Ser	Lys	Tyr	Gly	Ile		
170									75				80				85	
172	act	cat	aaa	gcg	ttt	gct	caa	ttt	ctt	ctg	gaa	aga	tat	aaa	tca	ttg		404
173	Thr	His	Lys	Ala	Phe	Ala	Gln	Phe	Leu	Arg	Glu	Arg	Tyr	Lys	Ser	Leu		
174									90			95				100		
176	aag	gac	ttg	aag	gat	gaa	ata	ttg	act	ctg	cat	ttc	agt	ctc	aag	gag		452
177	Lys	Asp	Leu	Lys	Asp	Glu	Ile	Leu	Thr	Arg	His	Phe	Ser	Leu	Lys	Glu		
178									105			110				115		
180	atg	tct	act	ggg	tat	gaa	tta	atg	ggt	atg	cat	cg	ac	ata	caa	cat		500
181	Met	Ser	Thr	Gly	Tyr	Glu	Leu	Met	Gly	Met	His	Arg	Asn	Ile	Gln	His		
182									120			125				130		
184	cga	gtg	gat	ttc	ttg	gaa	tgg	gct	cca	ggt	gct	cg	tc	tgt	gct	ctg		548
185	Arg	Val	Asp	Phe	Leu	Glu	Trp	Ala	Pro	Gly	Ala	Arg	Tyr	Cys	Ala	Leu		
186									135			140				145		150
188	att	gg	tac	ttc	aat	ggg	tgg	tca	aca	act	gg	at	tgt	gcc	aga	gag		596
189	Ile	Gly	Asp	Phe	Asn	Gly	Trp	Ser	Thr	Thr	Gly	Asn	Cys	Ala	Arg	Glu		
190									155			160				165		
192	gg	cat	ttt	gg	cat	gac	gat	tat	ggg	tat	tgg	ttt	att	att	ctt	gaa		644
193	Gly	His	Phe	Gly	His	Asp	Asp	Tyr	Gly	Tyr	Trp	Phe	Ile	Ile	Leu	Glu		
194									170			175				180		
196	gat	aaa	tta	cgt	gaa	gga	gaa	gaa	cct	gat	aaa	ttg	tat	ttt	caa	cag		692
197	Asp	Lys	Leu	Arg	Glu	Gly	Glu	Glu	Pro	Asp	Lys	Leu	Tyr	Phe	Gln	Gln		
198									185			190				195		
200	tac	aat	tat	g	cg	g	g	ac	t	at	g	at	aa	g	cc	gt		740
201	Tyr	Asn	Tyr	Ala	Glu	Asp	Tyr	Asp	Lys	Gly	Asp	Thr	Gly	Ile	Thr	Val		
202									200			205				210		
204	gag	gaa	atc	ttt	aaa	aaa	gca	aat	gat	gag	tat	tgg	gaa	cct	gga	gaa		788
205	Glu	Glu	Ile	Phe	Lys	Lys	Ala	Asn	Asp	Glu	Tyr	Trp	Glu	Pro	Gly	Glu		
206									215			220				225		230
208	gat	cgc	ttc	att	aaa	tca	cgt	tat	gag	gtg	gca	gca	aag	tta	tat	gag		836
209	Asp	Arg	Phe	Ile	Lys	Ser	Arg	Tyr	Glu	Val	Ala	Ala	Lys	Leu	Tyr	Glu		
210									235			240				245		
212	gaa	atg	ttc	g	g	cc	aa	t	g	at	ttt	g	aa	ct	aa	g		884
213	Glu	Met	Phe	Gly	Pro	Asn	Gly	Pro	Gln	Thr	Glu	Glu	Leu	Glu	Ala			
214									250			255				260		
216	atg	cct	gat	gca	g	c	aa	c	ta	cc	aa	gg	aa	cc	aa	aa		932
217	Met	Pro	Asp	Ala	Ala	Thr	Arg	Tyr	Lys	Thr	Trp	Lys	Glu	Gln	Gln	Lys		
218									265			270				275		
220	aag	gat	ccg	gca	agc	aat	ttg	cc	tcg	tat	gat	gtg	gta	gat	agt	gga		980
221	Lys	Asp	Pro	Ala	Ser	Asn	Leu	Pro	Ser	Tyr	Asp	Val	Val	Asp	Ser	Gly		
222									280			285				290		
224	aaa	gaa	tat	gat	att	ta	c	aa	ttt	g	at	cct	gaa	tc	ttt	aag		1028
225	Lys	Glu	Tyr	Asp	Ile	Tyr	Asn	Ile	Ile	Gly	Asp	Pro	Glu	Ser	Phe	Lys		
226									295			300				305		310
228	aaa	ttt	cgt	atg	aaa	cag	cct	cct	att	gct	tac	tgg	tta	gaa	act	aaa		1076

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229	Lys Phe Arg Met Lys Gln Pro Pro Ile Ala Tyr Trp Leu Glu Thr Lys			
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232	aag gga agg aaa ggc tgg tta cag aaa tat atg cct gct tta cct cat			1124
233	Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr Met Pro Ala Leu Pro His			
234	330	. 335	340	
236	gga agc aaa cac agg gtg tat ttt aac aca cca aat ggg cct ctt gaa			1172
237	Gly Ser Lys His Arg Val Tyr Phe Asn Thr Pro Asn Gly Pro Leu Glu			
238	345	350	355	
240	cga gtt cct gcg tgg gcc aat ttt gtc att cca gat gca gac ggg atg			1220
241	Arg Val Pro Ala Trp Ala Asn Phe Val Ile Pro Asp Ala Asp Gly Met			
242	360	365	370	
244	gca tta gca gtc cat tgg gaa cca cct cct gaa tat gct tat aaa tgg			1268
245	Ala Leu Ala Val His Trp Glu Pro Pro Glu Tyr Ala Tyr Lys Trp			
246	375	380	385	390
248	aaa cac aag cta cca gtc aag cct aag tcc ttg cgc ata tat gaa tgt			1316
249	Lys His Lys Leu Pro Val Lys Pro Lys Ser Leu Arg Ile Tyr Glu Cys			
250	395	400	405	
252	cat gtt ggc atc tct ggc cag gaa cca aaa gtt tca tct ttc aat gat			1364
253	His Val Gly Ile Ser Gly Gln Glu Pro Lys Val Ser Ser Phe Asn Asp			
254	410	415	420	
256	ttt att agc aag gtc ctt ccg cat gta aaa gaa gct gga tac aat gca			1412
257	Phe Ile Ser Lys Val Leu Pro His Val Lys Glu Ala Gly Tyr Asn Ala			
258	425	430	435	
260	acg caa att att gga gtt gtt gag cac aag gat tat ttc act gtt gga			1460
261	Thr Gln Ile Ile Gly Val Val Glu His Lys Asp Tyr Phe Thr Val Gly			
262	440	445	450	
264	tat aga gtg acc aat ttt tat gct gtt agt agc cgt tat ggc aca ccg			1508
265	Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser Ser Arg Tyr Gly Thr Pro			
266	455	460	465	470
268	gat gac ttc aag cgc ttg gtt gat gaa gca cat ggg ctt gga ctg ctt			1556
269	Asp Asp Phe Lys Arg Leu Val Asp Glu Ala His Gly Leu Gly Leu Leu			
270	475	480	485	
272	gtc ttt ttg gag att gtg cac tcc tat gca gca gca gat gaa atg gtt			1604
273	Val Phe Leu Glu Ile Val His Ser Tyr Ala Ala Ala Asp Glu Met Val			
274	490	495	500	
276	ggg tta tct ctt ttt gat gga gca aat gat tgc tat ttc cac act ggt			1652
277	Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp Cys Tyr Phe His Thr Gly			
278	505	510	515	
280	aaa cgt gga cac cac aaa ttc tgg ggc aca cgg atg ttc aaa tat gga			1700
281	Lys Arg Gly His His Lys Phe Trp Gly Thr Arg Met Phe Lys Tyr Gly			
282	520	525	530	
284	gat cct gat gtt ctg cac ttt ctt tca aat ctg aac tgg tgg gtg			1748
285	Asp Pro Asp Val Leu His Phe Leu Leu Ser Asn Leu Asn Trp Trp Val			
286	535	540	545	550
288	gag gag tat cat gtc gat ggc ttc cat ttt cat tcg ctc tcg tcc atg			1796
289	Glu Glu Tyr His Val Asp Gly Phe His Phe His Ser Leu Ser Ser Met			
290	555	560	565	
292	ttg tat acg cat aat gga ttt gct tca ttt act ggt gac atg gat gaa			1844
293	Leu Tyr Thr His Asn Gly Phe Ala Ser Phe Thr Gly Asp Met Asp Glu			

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294	570	575	580	
296	tac tgt aac caa tat gtt gac aag gag gcc tta ttg tac ctc ata tta			1892
297	Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala Leu Leu Tyr Leu Ile Leu			
298	585	590	595	
300	gca aat gaa gta tta cat gct ctt cat cct aat gtg atc acg att gct			1940
301	Ala Asn Glu Val Leu His Ala Leu His Pro Asn Val Ile Thr Ile Ala			
302	600	605	610	
304	gtg gat gca act ctg tat cct gga ctc tgc gat cca aca tct caa ggt			1988
305	Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys Asp Pro Thr Ser Gln Gly			
306	615	620	625	630
308	gga ctg ggc ttt gat tat ttt gcc aat ctt tct gcc tca gag atg tgg			2036
309	Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu Ser Ala Ser Glu Met Trp			
310	635	640	645	
312	cct gca tta ctt gaa aat act cct gat cat gaa tgg tgc atg agt aag			2084
313	Leu Ala Leu Leu Glu Asn Thr Pro Asp His Glu Trp Cys Met Ser Lys			
314	650	655	660	
316	att gtt agc aca tta gtg ggc gat aga caa aat act gat aaa atg ctt			2132
317	Ile Val Ser Thr Leu Val Gly Asp Arg Gln Asn Thr Asp Lys Met Leu			
318	665	670	675	
320	ttg tat gca gaa aat cac aac cag tcc att tct gga ggt cgt tcc ttc			2180
321	Leu Tyr Ala Glu Asn His Asn Gln Ser Ile Ser Gly Gly Arg Ser Phe			
322	680	685	690	.
324	gca gaa ata ctg att ggt aac tcc ttg ggg aaa tct tcc ata tca caa			2228
325	Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly Lys Ser Ser Ile Ser Gln			
326	695	700	705	710
328	gag tca tta ctt aga ggc tgc tcg tta cac aag atg atc aga tta att			2276
329	Glu Ser Leu Leu Arg Gly Cys Ser Leu His Lys Met Ile Arg Leu Ile			
330	715	720	725	
332	aca tct aca att ggt ggt cat gca tac ctc aac ttc atg ggc aat gaa			2324
333	Thr Ser Thr Ile Gly Gly His Ala Tyr Leu Asn Phe Met Gly Asn Glu			
334	730	735	740	
336	ttt ggt cac cca aag aga gta gag ttt cca atg tca agc aac aat ttc			2372
337	Phe Gly His Pro Lys Arg Val Glu Phe Pro Met Ser Asn Asn Phe			
338	745	750	755	
340	tcc ttt tca ctg gct aac cgt cgc tgg gat cta ttg gaa gat gtt gta			2420
341	Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp Leu Leu Glu Asp Val Val			
342	760	765	770	
344	cat tat caa tta ttc tca ttt gat aag gat atg atg gac ttg gat aaa			2468
345	His Tyr Gln Leu Phe Ser Phe Asp Lys Asp Met Met Asp Leu Asp Lys			
346	775	780	785	790
348	aat ggg aga att ttg tcc aga ggt ctt gcc aac att cac cat gtc aat			2516
349	Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala Asn Ile His His Val Asn			
350	795	800	805	
352	gat act acc atg gtg att tct tac ttg aga ggt ccc aat ctc ttt gtg			2564
353	Asp Thr Thr Met Val Ile Ser Tyr Leu Arg Gly Pro Asn Leu Phe Val			
354	810	815	820	
356	tcc aac ttt cat cct gtc aat tca tat gaa aga tac att ata ggt gtg			2612
357	Phe Asn Phe His Pro Val Asn Ser Tyr Glu Arg Tyr Ile Ile Gly Val			
358	825	830	835	

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date